

BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

SEQ ID NO: 3

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|11229

Description

None

Molecule type

nucleic acid

Query Length

21

Subject ID

gi|1914699|emb|X98077.1|

Description

Hepatitis B virus complete genome, wild type

Molecule type

nucleic acid

Subject Length

3215

Program

BLASTN 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters


Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Effective search space 44912

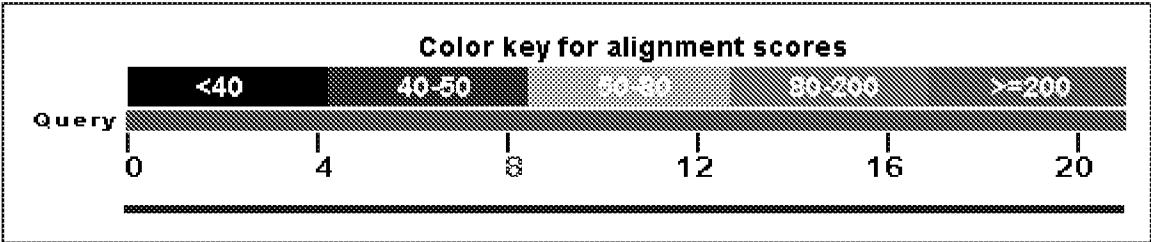
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[Graphic Summary](#)

Distribution of 8 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Dot Matrix View 

Plot of lcl|11229 vs gi|1914699|emb|X98077.1

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.




Descriptions

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

x98077.1	Hepatitis B virus complete genome, wild type	42.1	154	100%	9e-09	100%
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[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>**emb|x98077.1|** Hepatitis B virus complete genome, wild type
Length=3215

Sort alignments for this subject seq
E value **Score** **Percent identity**
Query start position **Subject star**

Score = 42.1 bits (21), Expect = 9e-09
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Minus

```
Query 1      GTGCAGAGGTGAAGCGAAGTG 21
          |||
Sbjct 1602    GTGCAGAGGTGAAGCGAAGTG 1582
```

Score = 22.3 bits (11), Expect = 0.009
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

```
Query 3      GCAGAGGTGAA 13
          |||
Sbjct 1834    GCAGAGGTGAA 1824
```

Score = 16.4 bits (8), Expect = 0.54
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Minus

```
Query 2      TGCAGAGG 9
          |||
Sbjct 410     TGCAGAGG 403
```

Score = 16.4 bits (8), Expect = 0.54
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Minus

```
Query 6      GAGGTGAA 13
          |||
Sbjct 2051    GAGGTGAA 2044
```

Score = 14.4 bits (7), Expect = 2.1
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

```
Query 3      GCAGAGG 9
          |||
Sbjct 1261    GCAGAGG 1255
```

Score = 14.4 bits (7), Expect = 2.1
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

```
Query 5      AGAGGTG 11
          |||
Sbjct 1533    AGAGGTG 1527
```

Score = 14.4 bits (7), Expect = 2.1
Identities = 7/7 (100%), Gaps = 0/7 (0%)

Strand=Plus/Minus

```
Query   3      GCAGAGG   9
        |||||
Sbjct   2007  GCAGAGG   2001
```

Score = 14.4 bits (7), Expect = 2.1
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

```
Query   5      AGAGGTG   11
        |||||
Sbjct   3182  AGAGGTG   3176
```

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)